



AMDR/C

SEQUENCE LISTING

<110> De Buyl, Eric
Lahaye, Andree
Ledoux, Pierre
Detroz, Rene

~~H 3~~

<120> Xylanase, Microorganisms Producing it,
DNA Molecules, Methods for Preparing this Xylanase and Uses
of the Latter

<130> GC450-D1-US

<140> US 09/909,207
<141> 2001-07-19

<150> US 08/470,953
<151> 1995-06-06

<150> BE 09500448
<151> 1995-05-17

<150> BE 09400706
<151> 1994-07-26

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caacaagg	gtaacatgtc	cataaactac	ggagccaaact	tccaacccaa	tggtaatgcg	240
tatttatgcg	tctatggttg	gactgttgc	cctcttgcg	aatattatat	tgtcgacagt	300
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tttaaacaat	attggagtgt	tgcagatcg	aaacgcacga	gtggcacgat	ttctgtcagc	480
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cttactgttag	aaggctatca	aagttagcgg	agtgtcaatg	tatatacgaa	tacactaaga	600
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gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat	96
Glu Phe Trp Lys Asp Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His	
20 25 30	
ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc	144
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe	
35 40 45	
cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa gtt ggt	192
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly	
50 55 60	
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Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala	
65 70 75 80	
tat tta tgc gtc tat ggt tgg act gtt gac cct ctt gtc gaa tat tat	288
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr	
85 90 95	
att gtc gac agt tgg ggc aac tgg cgt cca cca gga gca acg cct aag	336
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys	
100 105 110	
ggg acc atc act gtt gat gga gga aca tat gat atc tac gag act ctt	384
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu	
115 120 125	
aga gtc aat caa ccc tcc att aag ggg att gcc aca ttt aaa caa tat	432
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr	
130 135 140	
tgg agt gtt cga aga tcg aaa cgc acg agt ggc acg att tct gtc agc	480
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser	
145 150 155 160	
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Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met	
165 170 175	
tat gaa gtc gcg ctt act gta gaa ggc tat caa agt agc gga agt gct	576
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala	
180 185 190	
aat gta tat agc aat aca cta aga att aac ggt aac cct ctc tca act	624
Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr	
195 200 205	
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35 40 45
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly
50 55 60
Asn Met Ser Ile Asn Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala
65 70 75 80
Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr
85 90 95
Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys
100 105 110
Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu
115 120 125
Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr
130 135 140
Trp Ser Val Arg Arg Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser
145 150 155 160
Asn His Phe Arg Ala Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met
165 170 175
Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala
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195 200 205
Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn
210 215 220

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tatgattatg aattttggaa agatagcgtt ggctctggaa caatgattct caatcatggc 180
ggta cgttca gtgccaaatg gaacaatgtt aacaacatata tattccgtaa aggtaaaaaa 240
ttcaatgaaa cacaacacaca ccaacaagg t gtaacatgtt ccataaacta cggagccaaac 300
ttccaaccaa atggtaatgc gtat ttagtgc gtctatggtt ggactgttga cccttgc 360
gaatattata ttgtcgacag ttggggcaac tggcgccac caggagcaac gcctaagggg 420
accatcactg ttgatggagg aacatatgtt atctacgaga ctcttagagt caatcaaccc 480
tc cattaagg ggattgccc acat taaaacaa tattggagtg ttcaagatc gaaacgcacg 540
agtggcacga ttctgtcag caaccactt agagcgtggg aaaacttagg gatgaatatg 600
ggaaaaatgt atgaagtgc gcttactgta gaaggctatc aaagtgcgg aagtgcataat 660
gtatatacgca atacactaag aattaacgtt aaccctctt caactattag taatgacgag 720
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gca cta acc tta cct gca gaa ata att cag gca caa atc gtc acc gac 96
Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala Gln Ile Val Thr Asp
20 25 30
aat tcc att ggc aac cac gat ggc tat gat tat gaa ttt tgg aaa gat 144
Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp
35 40 45
agc ggt ggc tct ggg aca atg att ctc aat cat ggc ggt acg ttc agt 192
Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser
50 55 60
gcc caa tgg aac aat gtt aac aac ata tta ttc cgt aaa ggt aaa aaa 240
Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys
65 70 75 80
ttc aat gaa aca caa aca cac caa caa gtt ggt aac atg tcc ata aac 288
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn
85 90 95
tac gga gcc aac ttc caa cca aat ggt aat gcg tat tta tgc gtc tat 336
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr
100 105 110
ggg tgg act gtt gac cct ctt gtc gaa tat tat att gtc gac agt tgg 384
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp
115 120 125
ggc aac tgg cgt cca cca gga gca acg cct aag ggg acc atc act gtt 432
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val
130 135 140
gat gga gga aca tat gat atc tac gag act ctt aga gtc aat caa ccc 480
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro
145 150 155 160
tcc att aag ggg att gcc aca ttt aaa caa tat tgg agt gtt cga aga 528
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg
165 170 175
tcg aaa cgc acg agt ggc acg att tct gtc agc aac cac ttt aga gcg 576
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala
180 185 190
tgg gaa aac tta ggg atg aat atg ggg aaa atg tat gaa gtc gcg ctt 624
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu

195

200

205

act gta gaa ggc tat caa agt agc gga agt gct aat gta tat agc aat	672																
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn																	
210	215	220		aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag	720	Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu		225	230	235	240	agc ata act ttg gat aaa aac aat	744	Ser Ile Thr Leu Asp Lys Asn Asn		245	
220																	
aca cta aga att aac ggt aac cct ctc tca act att agt aat gac gag	720																
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu																	
225	230	235	240	agc ata act ttg gat aaa aac aat	744	Ser Ile Thr Leu Asp Lys Asn Asn		245									
235	240																
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<213> *Bacillus* sp.

<400> 6

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Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr Glu Phe Trp Lys Asp			
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Ser Gly Gly Ser Gly Thr Met Ile Leu Asn His Gly Gly Thr Phe Ser			
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Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe Arg Lys Gly Lys Lys			
65	70	75	80
Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly Asn Met Ser Ile Asn			
85	90	95	
Tyr Gly Ala Asn Phe Gln Pro Asn Gly Asn Ala Tyr Leu Cys Val Tyr			
100	105	110	
Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr Ile Val Asp Ser Trp			
115	120	125	
Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys Gly Thr Ile Thr Val			
130	135	140	
Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu Arg Val Asn Gln Pro			
145	150	155	160
Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr Trp Ser Val Arg Arg			
165	170	175	
Ser Lys Arg Thr Ser Gly Thr Ile Ser Val Ser Asn His Phe Arg Ala			
180	185	190	
Trp Glu Asn Leu Gly Met Asn Met Gly Lys Met Tyr Glu Val Ala Leu			
195	200	205	
Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala Asn Val Tyr Ser Asn			
210	215	220	
Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr Ile Ser Asn Asp Glu			
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gca cta acc tta cct gca gaa ata att cag gca 81
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 <213> *Bacillus* sp.

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 gataattatc cagttcaaa atttgcataa gtgttatgg aatagttga atgtcaactg 540
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aaacttaggg atgaatatgg ggaaaatgtt tgaagtcgcg cttactgttag aaggctatca	1260
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ttcggttcaag ttctcattat tttcaaataa cctcccggtt ggatctttc caacgggagg	1440
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<221> sig_peptide
<222> (620)...(700)

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ataggaactt tcccatttgc aagacgataa aaaatctttt tcccctattt tatcttacg	180
ccttgcgtt tttttttttt aaactttttt tttagtttacg tgatgttccc tcattcatac	240
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ctgtgaaagg agggtaggta gtaccgtaga cttcattacc aaaaatttagt tgtaaaaaaa	600
ttaaaaggag gaatgccta atg aga caa aag aaa ttg acg ttg att tta gcc	652
Met Arg Gln Lys Lys Leu Thr Leu Ile Leu Ala	
1 5 10	

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Phe Leu Val Cys Phe Ala Leu Thr Leu Pro Ala Glu Ile Ile Gln Ala	
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Gln Ile Val Thr Asp Asn Ser Ile Gly Asn His Asp Gly Tyr Asp Tyr	
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gaa ttt tgg aaa gat agc ggt ggc tct ggg aca atg att ctc aat cat	796
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45 50 55	

ggc ggt acg ttc agt gcc caa tgg aac aat gtt aac aac ata tta ttc	844
Gly Gly Thr Phe Ser Ala Gln Trp Asn Asn Val Asn Asn Ile Leu Phe	
60 65 70 75	

cgt aaa ggt aaa aaa ttc aat gaa aca caa aca cac caa gtt ggt	892
Arg Lys Gly Lys Lys Phe Asn Glu Thr Gln Thr His Gln Gln Val Gly	
80 85 90	

aac atg tcc ata aac tac gga gcc aac ttc caa cca aat ggt aat gcg	940
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Tyr Leu Cys Val Tyr Gly Trp Thr Val Asp Pro Leu Val Glu Tyr Tyr			
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Ile Val Asp Ser Trp Gly Asn Trp Arg Pro Pro Gly Ala Thr Pro Lys			
125	130	135	
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Gly Thr Ile Thr Val Asp Gly Gly Thr Tyr Asp Ile Tyr Glu Thr Leu			
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Arg Val Asn Gln Pro Ser Ile Lys Gly Ile Ala Thr Phe Lys Gln Tyr			
160	165	170	
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175	180	185	
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190	195	200	
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Tyr Glu Val Ala Leu Thr Val Glu Gly Tyr Gln Ser Ser Gly Ser Ala			
205	210	215	
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Asn Val Tyr Ser Asn Thr Leu Arg Ile Asn Gly Asn Pro Leu Ser Thr			
220	225	230	235
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Ile Ser Asn Asp Glu Ser Ile Thr Leu Asp Lys Asn Asn			
240	245		
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ataggaactt tcccatttgc aagacgataa aaaatctttt tcccatttt tatcttatcg			180
ccttgatcggtttaatttgc aactttattttttagtttacg tgatgttccc tcattcatac			240
cattaatcac agttaacgct agagtcatact ttttcgggtt ctcaaaaata cctgaagaac			300
atttatgtca tattttctca cggccgttcca taatggata tatatactct tttatacata			360
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gataattatac cagtttcaaa atttggaaata gtgtgtatgg aatagtttga atgtcaactg			540
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ttaaaaggag gaatgcctaa			619

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic oligonucleotide

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<210> 15
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<220>
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